

SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine
microorganism, paracoccus haeundaesis, producing the
carotenoid

<130> 428.1056

<140> US 10/551,508
<141> 2005-09-29

<150> PCT/KR2004/000752
<151> 2003-03-31

<150> KR2003-20222
<151> 2003-03-31

<150> KR2003-20023
<151> 2003-03-31

<160> 18

<170> KopatentIn 1.71

<210> 1
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for Paracoccus haeundaesis 16S rDNA

<400> 1
cataagtaat tatggttttg t 21

<210> 2
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for Paracoccus haeundaesis 16S rDNA

<400> 2
cgcttcctta gaaaggag 18

<210> 3
<211> 1454
<212> DNA

<213> Paracoccus haeundaesis

<400> 3
caacttgaga gtttgatcct ggctcagaac gaacgctggc ggcaggctta acacatgcaa 60
gtcgagcgag accttcgggt cttagccggg acgggtgagt aacgcgtggg aacgtgccct 120
tctctacgga atagccccgg gaaactggga gtaataccgt atacgcccctt tgggggaaag 180
atttatcgga gaaggatcgg cccgcgttgg attaggttgt tggtgggtt atggccacc 240
aagccgacga tccatagctg gtttgagagg atgatcagcc acactgggac tgagacacgg 300
cccagactcc tacgggaggc agcagtgggg aatcttagac aatgggggca accctgatct 360
agccatgccc cgtgagtgtat gaaggcctta gggttgtaaa gctcttcag ctggaaagat 420
aatgacggta ccagcagaag aagccccggc taactccgtg ccagcagccg cggttaatacg 480
gagggggcta gcgttgcgttgcg gaattactgg gcgtaaagcg cacgtggcgcg gactggaaag 540
tcagaggtga aatcccaggc ctcaaccttg gaactgcctt tgaaactatc agtctggagt 600
tcgagagagg tgagtggaaat tccgagtgtt gaggtgaaat tcgtagatat tcggaggaac 660
accagtggcg aaggcggctc actggctcga tactgacgct gaggtgcgaa agcgtgggga 720
gcaaaacagga ttagatacc tggtagtcca cggcgtaaac gatgaatgcc agacgtccgc 780
aagcatgctt gtcgggtgtca cacctaacgg attaagcatt ccgcctgggg agtacggcgt 840
caagattaaa actcaaagga attgacgggg gcccgcacaa gcgggtggagc atgtggttta 900
attcgaagca acgcgcagaa ctttaccaac ctttgacatg gcaggaccgc tggagagatt 960
cagctttctc gtaagagacc tgcacacagg tgctgcatttgc ctgtcgtag ctgtgtcgt 1020
gagatgttcg gttaagtccg gcaacgagcg caacccacgt ccctagttgc cagcattcag 1080
ttgggcactc tatggaaact gcccgtata agtcggagga aggtgtggat gacgtcaagt 1140
tctcatggcc cttacgggtt gggctacaca cgtgctacaa tgggtggtagt agtgggttaa 1200
tccccaaaag ccatctcagt tcggattgtc ctctgcaact cgagggcatg aagttggaaat 1260
cgctagtaat cgccgaacag catgccgcgg tgaatacgctt cccgggcctt gtacacaccg 1320
cccgtcacac catgggagtt ggttctaccc gacgacgctg cgctaacctt cggggggcag 1380
gcggccacgg taggatcagc gactgggtg aagtcgttaac aaggtagccg taggggaacc 1440
tgccggctggta tcac 1454

<210> 4
<211> 6223
<212> DNA

<213> crt gene

<400> 4
gttccacgac tggggcatcc ccaegaccgc gtcgctgcgc gccatcgccc cgatgatggg 60
gcgggaccgg gttctggtcg ggtcgccgg ggtcgctcac gggctggacg ccgcgcgggc 120
catccgcctc ggccggacc tcgtggggca ggcggccccc gcgcgtcccc ccgcgcgc 180
cagcggcggag gcccgtccg atcacctgtc cgacgtcgta acccagctgc gcacgcgat 240
gttctgcacc ggatcggggcg accttgcagg gctgcgtgc gcgcctctgc tggtgccgg 300
gcgggtggc caatggtcgc aagcaacggg gatggaaacc ggcatgcgg gactgttagtc 360
tgccggatc gccggtccgg gggacaagat gagcgcacat gcccgtccca aggcaagatct 420
gaccggcacc agcctgatcg ttcggggccg catcatgcgc gctggctgg ccctgcatt 480
gcacgcgtg tggtttctgg acgcggccggc gcacccatc ctggcgatcg cgaatttcct 540
ggggctgacc tggctgtcgg tcggctgtt cttcatgcgc catgacgcga tgcacgggtc 600
ggtcgtgcgg gggcgteccgc gggcaatgc ggcatgggc cagctggtcc tgtggctgt 660
tgccggattt tcgtggcgca agatgatcgt caagcacatg gcccattacc gccataccgg 720
aaccgacgac gaccccgatt tcgaccatgg cggcccggtc cgctggta cgccgttcat 780
cgccacccat ttccggctggc gcgaggggct gctgctgccc gtcacgtga cggctatgc 840
gctgatccctg ggggatcgtt ggtatgtacgt ggttttctgg ccgcgtccgt cgatccctggc 900
gtcgatccag ctgttcgtgt tcggcacctg gtcggccgcac cgcccccggcc acgacgcgtt 960
cccgaccgc cataatgcgc ggtcgccgc gatcagccgc cccgtgtcgc tgctgaccc 1020
ctttcacttt ggtggttatc atcacgaaca ccacctgcac ccgacgggtc cttggtgccg 1080
cctgcccagg acccgccacca agggggacac cgcatgacca attccctgtat cgtcgtcgcc 1140
accgtgtctgg tcatggagtt gacggcctat tccgtccacc gttggatcat gcacggcccc 1200
ctgggctggg gctggcaca gtcaccac gagaaacacg accacgcgtt ggaaaagaac 1260
gacctgtacg gcctggtctt tcgggtgatc gtcacgggtc tggatggatc gggctggatc 1320
tggcgccgg tcctgtggtg gatcgctttg ggcacgtaccc tctatgggt gatctatttc 1380
gtccctgcattt acgggctgtt tcatcagccgc tggccgttcc gtcataatccc ggcacggcc 1440
tatgcggccgc gcctgtatca ggccaccgc ctgcaccacg cggtcgagggg acgacgaccat 1500
tgccgtcagtt tcggcttcat ctatgcgcgc ccgggtcgaca agctgaagca ggacactgaag 1560
acgtcgccggcg tgctgcgggc cgaggccgcag gagcgcacgt gacccatgac gtgctgtgg 1620

caggggcggg ctttgcgaac gggctgtatcg ccctggcgct gcgcgcggcg cggcccgacc 1680
tgccccgtct gctgttgtat catgcggcgg gaccgtcaga cggccataacc tggtcctgcc 1740
acgaccccgaa tctgtcgccg cactggctgg cgccggctgaa gcccctgcgc cgcccaact 1800
ggcccgacca ggaggtgcgc tttccccgcc atgcggcgct gctggccacc ggttacgggt 1860
cgctggacgg ggccggcgctg gcggatgcgg tggcccggtc gggccgcgag atccgctgga 1920
acagcgacat cgccctgtcgat gatgaacagg gggcgacgct gtcctgcggc acccgatcg 1980
aggcgccgc ggtccctggac gggcgccgcg cgccggcgctc gccggatctg accgtgggtt 2040
tccagaaatt cgtggcgctc gagatcgaga ccgactgccc ccacggcgta ccccgccgaa 2100
tgatcatgga cgccggcgctc acccagcagg acgggtaccg attcatctat ctgctgccct 2160
tctctccgac gccatcctg atcgaggaca ctcgctattc cgatggcgcc aatctggacg 2220
acgacggcgct ggcggcgccg tcccacgact atgcggccca gcagggtctgg accggggccg 2280
aggtccggcg cgaacgcggc atccctgccc ttgcgtggc ccatgacgcg gcgggcttct 2340
ggggccgatca cgccggagggg cctgttcccg tggactgcg cgccgggttc tttcacccgg 2400
tcacccggcta ttgcgtgccc tatgcggcgcc aggtggcgga cgtgggtggcg ggccctgtccg 2460
ggcccgcccg caccgacgcg ctgcgcggcg ccatccgcga ttacgcgtc gaccgggcac 2520
gcggcgatcg ctttctgcgc ctgctgaacc ggatgtcttt ccggcgctgc gcggccgacc 2580
ggcgctatac cctgctgcag cgggttctacc gcatgcgcga tggactgatc gaacggttct 2640
atgcggcccg gctgagcgctg gcggatcgcg tgccatcgat gacccggcaag cctccattc 2700
cccttggcac ggccatccgc tgccatccccg aacgtccccct gctgaaggaa aacgcatgaa 2760
cgcccatcg cccgcggcca agaccgcatt cgtgatcgcc gcaggcttgc gcgggctggc 2820
cctggccatc cgccctgcagt ccgcggcat cgccaccacc ctggtcgagg cccgggacaa 2880
gccccgggg cgccgcctatg tctggcacga tcagggccat gtcttcgacg cggggcccgac 2940
cgtcatcacc gaccccgatg cgctcaagga gctgtggcg ctgaccgggc aggacatggc 3000
gcgcgcacgtg acgctgtatgc cgggtgtcgcc cttctatcga ctgatgtggc cggggccggaa 3060
ggtcttcgat tacgtgaacg aggccgatca gctggagcg cagatgcgcc agttcaaccc 3120
ggacgacctg gaaggatacc gcccgttccg tgattacgcg gaggaggtgt atcaggaggg 3180
ctacgtcaag ctgggcaccg tgcccttcct caagctgggc cagatgtca aggccgcgc 3240
cgccgtatcg aagctggagg cctataagtc cgtccatgcc aagggtcgca ctttcatcaa 3300
ggacccctat ctgcggcagg cggtttcgta tcacacgctg ctgggtggcg ggaatccctt 3360

ctcgaccaggc tcgatctatg cgctgatcca cgcgcgtggag cggcgccggcg gggctctggtt 3420
cgccaaagggc ggcaccaacc agctggtcgc gggcatggtc gcgcgttgc aacggcttgg 3480
cggccagatg atgctgaacg ccaaggttcgc ccggatcgag accgagggcg cgcggaccac 3540
gggcgtcacc ctggcggacg ggcggtcttt aagggccgac atggtcgcca gcaacggcga 3600
cgtcatgcac aactatcgcg acctgtctggg ccacacggcc cgcgccgaga gccgcgcgaa 3660
atcgctggac cgcaagcgct ggtccatgtc gttgttcgtg ctgcatttcg gtctgcgcga 3720
ggcgcccaag gacatcgcg atcacaccat cctgttcggc ccccgctaca gggagctygt 3780
caacgagatc ttcaagggcc cgaagctggc cgaggatbtc tgcgtgtacc tgcattcgcc 3840
ctgcacgacc gatccggaca tggcgcttc gggcatgtcc aegcattacg tgctggcccc 3900
cgtgccgcat ctgggccgacg ccgagatcga ttgggcccgc gaggggccgc gctatgccga 3960
ccgcattctg gcgtccctgg aggagcggct gatcccgaac ctgcgcgcga acctgaccac 4020
gacgcgcata ttcacgcccc cgcatttcgc cagcgaactg aacgcgcatac acggcagcgc 4080
cttctcggtc gagccgatcc tgacgcaatc cgcgtggttc cggccgcaca accgcgcacaa 4140
gacgatccgc aacttctatc tggtcggcgc gggcaccat cggggcgogg gcattccggg 4200
cgtegtggc tcggccaagg ccacggccca ggtgatgtc tccgacctgg cgggcgcatg 4260
agegatctgg tcctgaccc gacggaggcg atcacccaaag ggtcgaaag ctttgccacg 4320
gcggccaagg tcatgcccgc gggcatccgc gacgacacgg tgatgtcta tgcctgggtc 4380
cgccacgcgg atgacgttat cgcgggtcag gccctggca gcccgcggcg ggccgtgaac 4440
gacccgcagg cgccggctgga cggcctgcgc gtcgacacgc tggccgcctt gcagggcgac 4500
ggtccgggtga ccccgccctt tgccgcgtc cgcgcgggtgg cgcggccgca tgatttcccg 4560
caggcctggc ccatggaccc gatcgaaggc ttgcgtatgg atgtcgaggc ggcgcactat 4620
cgcacgctgg atgacgtgt ggaatattcc tatcacgtcg caggcatcg cggcgatgt 4680
atggcccgcg tgatggcggt ggcgcacgt cctgtccctgg accgcgcctg cgacctgggg 4740
ctggcggtcc agctgaccaa catcgccgc gacgtgatcg acgtgcgcg catcgccgg 4800
tgctatctgc cgggggactg gctggaccag gcggggcgccg ggatcgacgg gcccggcg 4860
tcggccggagc tgtacacagt gatcctccgg ctgttggatg aggccgaacc ctattacgcg 4920
tcggccgggg tgggtctggc ggatctgcca cgcgcgtgcg cctggccat cgcgcgcgcg 4980
ctacggatct atcgccat cggcgtgcgc atccgcaaga gcggggccgc ggcctatcgc 5040

cagcggatca gcacgtccaa ggctgccaag atcggcctgc tggcgctgg gggctggat 5100
 gtgcgcgat cacgcctgcc gggggcgggc gtgtcgccgc agggcctctg gaccggccg 5160
 catcacgtct aggccgcgcgc ggcgttagggc agaacccttt ccagcaggcc cgcgatttcc 5220
 ggagcctgaa ggccgttgcgt ggcgcgcgc ggcgtccagtt gggcgccggct ggccctcgtaa 5280
 tgacgggaca cgttcgtcag gtctgacacg gccagaaggc cgccgcgcgg gcccggggcc 5340
 gccggcatcgc gaccggtatac cttgccaagc gccgcctggc cgcacgcac gtccagcagg 5400
 tcgtcatagg actggaacac gccccccagc tgacggccaa agtcgatcat ctgggtctgc 5460
 tcctcgccgt cgaactcctt gatcacggcc agcatctcca gcccggcgat gaacagcacg 5520
 ccggctttca ggtcctgttc ctgttcgacc cccgcgcgt tcttggccgc gtgcaggcgg 5580
 aggtcctggc cggcgcacag gcccgcggc cccagggacc ggcacaggat ccgcaccaggc 5640
 tgccgcgcga cctgtcccgaa cgccgcgcgc gcacggccca gcagggccat tgccctcggt 5700
 atcagggcga tgccgcccag cacggcacgg ctttcgcacatg ggtcgccggc 5760
 cggccgcggc gcaagccggc atcgtccatg cagggcaggt cgtcgaagat cagcgatgcg 5820
 gcatgcacca tctcgaccgc gcaggcggcg tcgacgatcg tgtcgcagac cccgcccgg 5880
 gcctctgccc caagcagcat cagcatgccg cggacccgc tgccgcacga cagcgccca 5940
 tggctcatgg ccgcgcggcag cggctgcgc acggcacccga atccctgggc gatctcttca 6000
 agtctggctt gcagaagggt ggcgtggatc gggttgacgt ctgcgtctcat cagtgccttc 6060
 ggcgttgggt tctgacctgg cggaaaggc aggcggggcc ggcaccccgat gaccgcgtcat 6120
 ccaccgtcaa cagtccccat gtttggacgg ttacgcacccg attgcgagcc ttttcgacgg 6180
 cgacgcgggg tcgcgcggca atttgtccaa caaggtcagt gga 6223

<210> 5
 <211> 729
 <212> DNA
 <213> crtW gene

<400> 5
 atgagcgcac atgcctgcc caaggcagat ctgaccgcac ccagcctgtat cgttcgggc 60
 ggcacatcatcg ccgcgtggct ggcctgcac gtgcacgcgc tgggtttct ggacgcggcg 120
 ggcacatccca tcctggcgat cgcgaatttc ctggggatga cctggctgtc ggtcggtctg 180
 ttcttcatcg cgcacgcgc gatgcacggg tcggtcgtgc cggggcgtcc ggcggcaat 240
 cggccgtatgg gcaagctggcgtt cctgtggctgtatgcggat ttgcgtggcg caagatgtc 300

gtcaaggcaca tggcccatca cgcataacc ggaaccgacg acgaccggga tttcgaccat 360
 ggccggccgg tccgctggta cgcgccgttc atcggcacct atttcggctg gcgcgagggg 420
 ctgctgtgc ccgtcatcggt gacggtctat gcgctgatcc tggggatcg ctggatgtac 480
 tggtcttctt ggccgctgcc gtcgatcctg gctcgatcc agctgttgtt gttcgccacc 540
 tggctgccgc accggccccgg ccacgacgacg ttccggacc gccataatgc gcggtcgtcg 600
 cggatcagcg accccgtgtc gctgctgacc tgctttact ttggtggtta tcacacgaa 660
 caccacactgc acccgacggt gccttggtgg cgctgcccgc acacccgcac caagggggac 720
 accgcatga 729

<210> 6
 <211> 242
 <212> PRT
 <213> crtW amino acid

<400> 6
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro

180	185	190
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu		
195	200	205
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His		
210	215	220
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp		
225	230	235
Thr Ala		

<210>	7	
<211>	489	
<212>	DNA	
<213>	crtZ gene	
<400>	7	
atgaccaatt tcctgatcggt cgtcgccacc gtgctggta tggagttgac ggcctattcc 60		
gtccaccgtt ggatcatgca cggccccctg ggctggggct ggcacaagtc ccaccacgag 120		
gaacacgacc acgcgctgga aaagaacgac ctgtacggcc tggtctttgc ggtgatcgcc 180		
acggtgctgt tcacggtggg ctggatctgg ggcgggtcc tgtggtggat cgctttggc 240		
atgaccgtct atgggctgat ctatttcgtc ctgcatgacg ggctggttca tcagcgctgg 300		
ccgttccgtat atatcccccgca caagggttat gcccggccgc tgtatcaggc ccaccggctg 360		
caccacgccc tcgagggacg cgaccattgc gtcagcttcg gttcatcta tgcggccggc 420		
gtcgacaaacg tgaaggcagga octgaagacg tcggcggtgc tgcggggcga ggccgaggag 480		
cgcacgtga 489		

<210>	8	
<211>	162	
<212>	PRT	
<213>	crtZ amino acid	
<400>	8	
Met Thr Asn Phe Leu Ile Val Val Ala Thr Val Leu Val Met Glu Leu 15		
1	5	10
15		

Thr Ala Tyr Ser Val His Arg Trp Ile Met His Gly Pro Leu Gly Trp		
20	25	30
Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys		
35	40	45
Asn Asp Leu Tyr Gly Leu Val Phe Ala Val Ile Ala Thr Val Leu Phe		
50	55	60

Thr Val Gly Trp Ile Trp Ala Pro Val Leu Trp Trp Ile Ala Leu Gly
65 70 75 80

Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
85 90 95

His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr Ala Arg
100 105 110

Arg Leu Tyr Gln Ala His Arg Leu His His Ala Val Glu Gly Arg Asp
115 120 125

His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
130 135 140

Lys Gln Asp Leu Lys Thr Ser Gly Val Leu Arg Ala Glu Ala Gln Glu
145 150 155 160

Arg Thr

<210> 9
<211> 1161
<212> DNA
<213> crtY gene

<400> 9
gtgacccatg acgtgctgct ggcagggcg ggccttgcga acgggctgat cgccctggcg 60
ctgcgcgcgg cgcggcccgaa cctgcgggtg ctgctgctgg atcatgcggc gggaccgtca 120
gacggccata cctggtcctg ccacgacccc gatctgtcgc cgcaactggct ggccgcggctg 180
aagccctgc gccgacgccaa ctggcccgac caggagggtgc gctttccccg ccatgccccgg 240
cggtctggcca ccggttacgg gtgcgtggac ggggcggcg tggcggatgc ggtggcccg 300
tcggggcgccg agatccgctg gaacagcgcac atcgccctgc tggatgaaca gggggccgacg 360
ctgtcctgcg gcacccggat cgaggcgggc ggggtctgg acgggcggcg cgccgcagccg 420
tcgcggcatt tgaccgtggg ttccagaaa ttctgtggcg tcgagatcga gaccgactgc 480
ccccacggcg tgcccccggcc gatgatcatg gacgcgaccg tcacccagca ggacgggtac 540
cgattcatct atctgctgcc ctctctccg acgcgcattc tgatcgagga cactcgctat 600
tccgatggcg gcaatctgga cgacgacgcg ctggcggcg cgtcccaacga ctatgcccgc 660
cagcagggt ggacccgggc cgaggtccgg cgccgaacgcg gcatccctgcc cattgcgtcg 720
gccccatgacg cggccggcatt ctggcccgat cacgcggagg ggcctgttcc cgtgggactg 780
cgccgcgggggt tctttcaccc ggtcacccggc tattcgctgc cctatgcggc gcaggtggcg 840

gacgtggtgg cgggcctgtc cggggccgccc ggcaccgacg cgctgctcgaa cgccatccgc 900
 gattacgcga tcgaccgggc acgcctgtac cgctttctgc gcctgctgaa ccggatgctg 960
 ttcccgccgt ggcgcggcga ccggcgctat accctgtctgc agcggttcta ccgcattgccg 1020
 catggactga tcgaacggtt ctatgcggc cggctgagcg tggcgatca gctgcgcata 1080
 gtgaccggca agcctcccat tcccccttggc acggccatcc gctgcctgcc cgaacgtccc 1140
 ctgctgaagg aaaacgcatt a 1161

<210> 10
 <211> 386
 <212> PRT
 <213> crtY amino acid

<400> 10
 Val Thr His Asp Val Leu Leu Ala Gly Ala Gly Leu Ala Asn Gly Leu
 1 5 10 15
 Ile Ala Leu Ala Leu Arg Ala Ala Arg Pro Asp Leu Arg Val Leu Leu
 20 25 30
 Leu Asp His Ala Ala Gly Pro Ser Asp Gly His Thr Trp Ser Cys His
 35 40 45
 Asp Pro Asp Leu Ser Pro His Trp Leu Ala Arg Leu Lys Pro Leu Arg
 50 55 60
 Arg Ala Asn Trp Pro Asp Gln Glu Val Arg Phe Pro Arg His Ala Arg
 65 70 75 80
 Arg Leu Ala Thr Gly Tyr Gly Ser Leu Asp Gly Ala Ala Leu Ala Asp
 85 90 95
 Ala Val Ala Arg Ser Gly Ala Glu Ile Arg Trp Asn Ser Asp Ile Ala
 100 105 110
 Leu Leu Asp Glu Gln Gly Ala Thr Leu Ser Cys Gly Thr Arg Ile Glu
 115 120 125
 Ala Gly Ala Val Leu Asp Gly Arg Gly Ala Gln Pro Ser Arg His Leu
 130 135 140
 Thr Val Gly Phe Gln Lys Phe Val Gly Val Glu Ile Glu Thr Asp Cys
 145 150 155 160
 Pro His Gly Val Pro Arg Pro Met Ile Met Asp Ala Thr Val Thr Gln
 165 170 175
 Gln Asp Gly Tyr Arg Phe Ile Tyr Leu Leu Pro Phe Ser Pro Thr Arg
 180 185 190
 Ile Leu Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asn Leu Asp Asp
 195 200 205

Asp Ala Leu Ala Ala Ala Ser His Asp Tyr Ala Arg Gln Gln Gly Trp
 210 215 220
 Thr Gly Ala Glu Val Arg Arg Glu Arg Gly Ile Leu Pro Ile Ala Leu
 225 230 235 240
 Ala His Asp Ala Ala Gly Phe Trp Ala Asp His Ala Glu Gly Pro Val
 245 250 255
 Pro Val Gly Leu Arg Ala Gly Phe Phe His Pro Val Thr Gly Tyr Ser
 260 265 270
 Leu Pro Tyr Ala Ala Gln Val Ala Asp Val Val Ala Gly Leu Ser Gly
 275 280 285
 Pro Pro Gly Thr Asp Ala Leu Arg Gly Ala Ile Arg Asp Tyr Ala Ile
 290 295 300
 Asp Arg Ala Arg Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu
 305 310 315 320
 Phe Arg Gly Cys Ala Pro Asp Arg Arg Tyr Thr Leu Leu Gln Arg Phe
 325 330 335
 Tyr Arg Met Pro His Gly Leu Ile Glu Arg Phe Tyr Ala Gly Arg Leu
 340 345 350
 Ser Val Ala Asp Gln Leu Arg Ile Val Thr Gly Lys Pro Pro Ile Pro
 355 360 365
 Leu Gly Thr Ala Ile Arg Cys Leu Pro Glu Arg Pro Leu Leu Lys Glu
 370 375 380

Asn Ala
 385

```

<210> 11
<211> 1506
<212> DNA
<213> crtI gene

<400> 11
atgaacgccc attcgcggc ggccaagacc gccatcgta tcggcgagg ctttggcgaa 60
ctggccctgg ccatccgcct gcagtccgcg ggcategcca ccaccctggc cgaggccccgg 120
gacaagccccg gccccggcgcc ctatgtctgg cacgatcagg gccatgtctt cgacgcgggc 180
ccgaccgtca tcaccgaccc cgatgcgcgc aaggagctgt gggcgctgac cgggcaggac 240
atggcgccgc acgtgacgct gatgccggtg tcgccttct atcgactgat gtggccgggc 300
gggaaggctt tcgattacgt gaacgaggcc gatcagctgg agcgcagat cgcccaagttc 360
aacccggacg accttggagg ataccggccgc ttccgtgatt acgcggagga ggtgtatcag 420
  
```

gagggctacg tcaagctggg caccgtgccc ttccctcaagc tgggccagat gctcaaggcc 480
 gcgcggcgcc tgatgaagct ggaggcctat aagtccgtcc atgccaaggt cgcgaccitc 540
 atcaaggacc cctatctgcg gcaggcgttt tcgtatcaca cgctgctggc gggcgaaaat 600
 cccttctcga ccagctcgat ctatgcgcgt atccacgcgc tggagcggcg cggcggggtc 660
 tggttcgcca agggcgacac caaccagctg gtgcgggca tggtcgcgt gttcaacgg 720
 cttggcgccc agatgtatgtc gaacgccaag gtgcgggca tcgagaccga gggcgccgg 780
 accacggcg tcaccctggc ggacgggccc tcttaaggc ccgacatggt cgccagcaac 840
 ggcgacgtca tgcacaacta tcgcacactg ctggccaca cggccccggc gcagagccgc 900
 gcgaaatcgc tggaccgcaa ggcgtggcc atgtcggtgt tcgtgcgtca ttccggctcg 960
 cgcgaggcgcc ccaaggacat cgcgcatcac accatcctgt tcggcccccg ctacagggag 1020
 ctggtcaacg agatcttcaa gggcccgaag ctggccgagg atttctcgct gtacctgcatt 1080
 tcgcacactgca cgaccgatcc ggacatggcg ctcggggca tgtccacgca ttacgtgcgt 1140
 gccccgtgc cgcatctggg cggcgccgag atcgattggg cggtcgaggg gcccgcgtat 1200
 gccgaccgca tcctggcgcc cctggaggag cggctgatcc cgaacctgcg cgccaacctg 1260
 accacgacgc gcatcttcac gcccggat ttgcgcagcg aactgaacgc ccatcacggc 1320
 agcgccttct cggtcgagcc gatectgacg caatccgcgt ggttccggcc gcacaaccgc 1380
 gacaagacga tccgcaactt ctatctggc ggcgcgggca cccatccggg cgccggcatt 1440
 cggggcgctcg tgggctcgcc caaggccacg gcccaggtga tgctgtccga ctcggcgccc 1500
 gcatga 1506

<210> 12
 <211> 501
 <212> PRT
 <213> crtI amino acid

<400> 12
 Met Asn Ala His Ser Pro Ala Ala Lys Thr Ala Ile Val Ile Gly Ala
 1 5 10 15

Gly Phe Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ser Ala Gly Ile
 20 25 30

Ala Thr Thr Leu Val Glu Ala Arg Asp Lys Pro Gly Gly Arg Ala Tyr
 35 40 45

Val Trp His Asp Gln Gly His Val Phe Asp Ala Gly Pro Thr Val Ile
 50 55 60

Thr	Asp	Pro	Asp	Ala	Leu	Lys	Glu	Leu	Trp	Ala	Leu	Thr	Gly	Gln	Asp
65															80
Met	Ala	Arg	Asp	Val	Thr	Leu	Met	Pro	Val	Ser	Pro	Phe	Tyr	Arg	Leu
					85					90					95
Met	Trp	Pro	Gly	Gly	Lys	Val	Phe	Asp	Tyr	Val	Asn	Glu	Ala	Asp	Gln
					100			105							110
Leu	Glu	Arg	Gln	Ile	Ala	Gln	Phe	Asn	Pro	Asp	Asp	Leu	Glu	Gly	Tyr
					115			120							125
Arg	Arg	Phe	Arg	Asp	Tyr	Ala	Glu	Glu	Val	Tyr	Gln	Glu	Gly	Tyr	Val
					130			135							140
Lys	Leu	Gly	Thr	Val	Pro	Phe	Leu	Lys	Leu	Gly	Gln	Met	Leu	Lys	Ala
					145			150			155				160
Ala	Pro	Ala	Leu	Met	Lys	Leu	Glu	Ala	Tyr	Lys	Ser	Val	His	Ala	Lys
					165			170							175
Val	Ala	Thr	Phe	Ile	Lys	Asp	Pro	Tyr	Leu	Arg	Gln	Ala	Phe	Ser	Tyr
					180			185							190
His	Thr	Leu	Leu	Val	Gly	Gly	Asn	Pro	Phe	Ser	Thr	Ser	Ser	Ile	Tyr
					195			200							205
Ala	Leu	Ile	His	Ala	Leu	Glu	Arg	Arg	Gly	Val	Trp	Phe	Ala	Lys	
					210			215							220
Gly	Gly	Thr	Asn	Gln	Leu	Val	Ala	Gly	Met	Val	Ala	Phe	Glu	Arg	
					225			230			235				240
Leu	Gly	Gly	Gln	Met	Met	Leu	Asn	Ala	Lys	Val	Ala	Arg	Ile	Glu	Thr
					245			250			255				255
Glu	Gly	Ala	Arg	Thr	Thr	Gly	Val	Thr	Leu	Ala	Asp	Gly	Arg	Ser	Leu
					260			265							270
Arg	Ala	Asp	Met	Val	Ala	Ser	Asn	Gly	Asp	Val	Met	His	Asn	Tyr	Arg
					275			280							285
Asp	Leu	Leu	Gly	His	Thr	Ala	Arg	Gly	Gln	Ser	Arg	Ala	Lys	Ser	Leu
					290			295			300				
Asp	Arg	Lys	Arg	Trp	Ser	Met	Ser	Leu	Phe	Val	Leu	His	Phe	Gly	Leu
					305			310			315				320
Arg	Glu	Ala	Pro	Lys	Asp	Ile	Ala	His	His	Thr	Ile	Leu	Phe	Gly	Pro
					325			330							335
Arg	Tyr	Arg	Glu	Leu	Val	Asn	Glu	Ile	Phe	Lys	Gly	Pro	Lys	Leu	Ala
					340			345							350
Glu	Asp	Phe	Ser	Leu	Tyr	Leu	His	Ser	Pro	Cys	Thr	Thr	Asp	Pro	Asp
					355			360			365				

Met Ala Pro Pro Gly Met Ser Thr His Tyr Val Leu Ala Pro Val Pro
 370 375 380
 His Leu Gly Arg Ala Glu Ile Asp Trp Ala Val Glu Gly Pro Arg Tyr
 385 390 395 400
 Ala Asp Arg Ile Leu Ala Ser Leu Glu Glu Arg Leu Ile Pro Asn Leu
 405 410 415
 Arg Ala Asn Leu Thr Thr Arg Ile Phe Thr Pro Ala Asp Phe Ala
 420 425 430
 Ser Glu Leu Asn Ala His His Gly Ser Ala Phe Ser Val Glu Pro Ile
 435 440 445
 Leu Thr Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile
 450 455 460
 Arg Asn Phe Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile
 465 470 475 480
 Pro Gly Val Val Gly Ser Ala Lys Ala Thr Ala Gln Val Met Leu Ser
 485 490 495
 Asp Leu Ala Gly Ala
 500

<210>	13					
<211>	915					
<212>	DNA					
<213>	crtB gene					
<400>	13					
atgagcgata	tggccctgac	ctcgaccgag	gcatcaccc	aagggtcgca	aagctttgcc	60
acggcggcca	agctgatgcc	gcggggcatc	cgcgacgaca	cggtgatgt	ctatgcctgg	120
tgcgcacacg	cggatgacgt	gatcgacggt	caggccctgg	gcagccgccc	cgaggcggtg	180
aacgacccgc	aggcgcggt	ggacggcctg	cgcgtcgaca	cgtggcgcc	cctgcagggc	240
gacggtccgg	tgaccccgcc	cattgcgcgc	ctgcgcgcgg	tggcgccggc	gcatgatttc	300
ccgcaggcct	gccccatgga	cctgatecgaa	ggcttcgcga	tggatgtcga	ggcgccgcac	360
tatcgacacgc	tggatgacgt	gttggatat	tcctatcact	tcgcaggcat	cgtcgccgtg	420
atgatggccc	gcgtgatgg	cgtgcgcgac	gatcctgtcc	tggaccgcgc	ctgcgacactg	480
gggctggcgt	tccagctgac	caacatcgcg	cgcgacgtga	tcgacgatgc	gcgcacatggg	540
cgggtgtatc	tgccggggga	ctggctggac	caggcgccgc	cgcggatcga	cggcccggtg	600
ccgtcgccgg	agctgtacac	agtgatccctc	cggctgttgg	atgaggcgga	accctattac	660

gcgtcggcgc gggtgtctt ggccatctg ccaccgcgtt gcgcctggtc catgcgcc 720
gcgcacggta tctatcgcc catcggttg cgcattccca agagcgggcc gcaggctat 780
cgccagcgta tcagcacgtt caaggctgcc aagatcgccc tgctgggcgtt cgggggctgg 840
gatgtcgccgatcacgcgtt gccggggcg ggcgtgtcgc ggcaggccct ctggaccgg 900
ccgcatcacttcttag 915

<210> 14
<211> 304
<212> PRT
<213> crtB amino acid

<400> 14
Met Ser Asp Leu Val Leu Thr Ser Thr Glu Ala Ile Thr Gln Gly Ser
1 5 10 15

Gln Ser Phe Ala Thr Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Asp
20 25 30

Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile
35 40 45

Asp Gly Gln Ala Leu Gly Ser Arg Pro Glu Ala Val Asn Asp Pro Gln
50 55 60

Ala Arg Leu Asp Gly Leu Arg Val Asp Thr Leu Ala Ala Leu Gln Gly
65 70 75 80

Asp Gly Pro Val Thr Pro Pro Phe Ala Ala Leu Arg Ala Val Ala Arg
85 90 95

Arg His Asp Phe Pro Gln Ala Trp Pro Met Asp Leu Ile Glu Gly Phe
100 105 110

Ala Met Asp Val Glu Ala Arg Asp Tyr Arg Thr Leu Asp Asp Val Leu
115 120 125

Glu Tyr Ser Tyr His Val Ala Gly Ile Val Gly Val Met Met Ala Arg
130 135 140

Val Met Gly Val Arg Asp Asp Pro Val Leu Asp Arg Ala Cys Asp Leu
145 150 155 160

Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp
165 170 175

Ala Arg Ile Gly Arg Cys Tyr Leu Pro Gly Asp Trp Leu Asp Gln Ala
180 185 190

Gly Ala Arg Ile Asp Gly Pro Val Pro Ser Pro Glu Leu Tyr Thr Val
195 200 205

Ile Leu Arg Leu Leu Asp Glu Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
210 215 220

Val Gly Leu Ala Asp Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala
225 230 235 240

Ala Leu Arg Ile Tyr Arg Ala Ile Gly Leu Arg Ile Arg Lys Ser Gly
245 250 255

Pro Gln Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
260 265 270

Gly Leu Leu Gly Val Gly Trp Asp Val Ala Arg Ser Arg Leu Pro
275 280 285

Gly Ala Gly Val Ser Arg Gln Gly Leu Trp Thr Arg Pro His His Val
290 295 300

<210> 15
<211> 882
<212> DNA
<213> crtE gene

<400> 15
atgagacgag acgtcaaccc gatccacgcc acccttctgc agaccagact tgaggagatc 60
gcccgaggat tcggtgccgt gtgcgcagccg ctcggcgccg ccatgagcca tggcgcgctg 120
tcgtcgccca ggcggttccg cggcatgctg atgctgcttg cggcagaggc ctggggcgccg 180
gtctgcgaca cgatcgatcg cggccctgc gcggtcgaga tggtgcatgc cgcatacgctg 240
atcttcgacg acctgccttg catggacgat gccgggctgc gccgcggccg gcccggccacc 300
catgtggcgc atggcgaaag ccgtgcgtg ctgggcggca tggccctgtat caccgaggca 360
atggccctgc tggccgggtgc gcgcggcccg tcgggcacgg tggggcgca gctggtgccg 420
atcctgtcgat ggtccctggg gccgcaggcc ctgtgcgcgg gccaggacct ggacctgcac 480
gcggccaaaga acggcgccgg ggtcgaacag gaacaggacc tgaagaccgg cgtgtgttc 540
atcgccgggc tggagatgtt ggcgtgtatc aaggagttcg acggccgagga gcagaccagg 600
atgatcgact ttggccgtca gctggccgcgtc gtgttccagt cctatgacga cctgtggac 660
gtcgtggcccg accaggccggc gcttggcaag gataccggtc gcgtatgcgcg ggcggccggc 720
ccgcggcccg gccttctggc cgtgtcagac ctgcagaacg tgtccctgtca ttacgaggcc 780
agccgcgcggc aactggacgc gatgtgcgc agcaagcgcc ttcaggctcc ggaaatcgcg 840
gcctgtgg aacgggttct gcctacgcc gcgcgcgcct ag 882

<210> 16
<211> 293
<212> PRT
<213> crtE amino acid

<400> 16
Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
1 5 10 15

Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
20 25 30

Ala Ala Met Ser His Gly Ala Leu Ser Ser Gly Arg Arg Phe Arg Gly
35 40 45

Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
50 55 60

Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80

Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly
85 90 95

Arg Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly
100 105 110

Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg
115 120 125

Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg
130 135 140

Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160

Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr
165 170 175

Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu
180 185 190

Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu
195 200 205

Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp
210 215 220

Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly
225 230 235 240

Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg
245 250 255

His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys
260 265 270

Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro
275 280 285

Tyr Ala Ala Arg Ala
290

<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for crt gene

<400> 17
gttccacgac tggggcatt 19

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for crt gene

<400> 18
tccactgacc ttgttgacaa attgccg 28